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Discrete time survival analysis of lamb mortality in a terminal sire composite population[1]

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ABSTRACT: Mortality records of 8,642 lambs from a composite population at the U.S. Meat Animal Research Center during the first year of life were studied using discrete survival analyses. Lamb mortality was studied across periods from birth to weaning, birth to 365 d of age, and weaning to 365 d of age. Animal–time data sets were created for each period using different time intervals: daily, weekly, fortnightly, and monthly. Each data set was analyzed using logistic and complementary log–log sire, animal, and maternal effects models. Explanatory variables included in the models were duration of time interval, sex, type of birth, contemporary group, age of dam, and type of upbringing (nursery or not). Similar estimates of explanatory variables were obtained within the same period across models and dif-
ferent time intervals. Heritability estimates from the complementary log–log models were greater than those from the comparable logistic models because of the difference in variance of the respective link functions. Heritability estimates from the complementary log–log sire model ranged from 0.13 to 0.21 for all periods. These estimates were greater than the complementary log–log animal model estimates that ranged from 0.04 to 0.12. Maternal effects were important early in life, with the maternal heritability slightly greater than the direct additive heritability. Negative correlations (−0.72 to −0.65) between direct additive and maternal effects was estimated. The similarity of results among survival analysis methods demonstrates that the discrete methodology is a viable alternative to estimate variance components in livestock survival data.

Key Words: Analysis, Heritability, Mortality, Sheep, Survival

Introduction

The survival of lambs is an important component of sheep production. Effective genetic improvement of lamb survival is based on accurate and precise estimates of genetic parameters. When lamb mortality has been analyzed as a cumulative binary variable to an arbitrary or predetermined time point, such as weaning, the resulting heritability estimates ranged between 0.0 and 0.1 (e.g., Fogarty, 1995; Lopez-Villalobos and Garrick, 1999). However, disadvantages of the cumulative binary approach include loss of information due to an arbitrary choice of period, failure to account for

censoring (animals leave the study before the event has occurred), and failure to account for covariate interactions with time or covariates that vary with time (Allison, 1997).

Continuous time survival analysis provides an alternative that overcomes many of the limitations of a cumulative binary approach (Allison, 1997). An empirical comparison of the continuous time and cumulative binary approaches reported by Southey et al. (2001) resulted in similar estimates of fixed effects, as anticipated by Ingram and Kleinman (1989) and Doskum and Gasko (1990). Southey et al. (2001) also reported that greater heritability estimates were obtained from the continuous time approaches than the cumulative binary approaches.

Often, the actual time of mortality is unavailable, but can be inferred by failure of an animal to appear for subsequent measurements. In this situation, the alternative discrete time methods can be used instead of the continuous time methods without the disadvantages of a cumulative binary approach. Discrete time methods do not require the specific time of mortality because an individual's survival history is defined by a set of discrete time intervals and can be analyzed using

1399

a binary regression model (Fahrmeir and Tutz, 1994; Allison, 1997). The objectives of this study were to apply discrete time methods to lamb mortality data using mixed effects models.

Materials and Methods

Description of Population and Management

Mortality was recorded on lambs from the F_3 and advanced generations of a terminal sire composite population (breed composition: 50% Columbia, 25% Hampshire, and 25% Suffolk) at the U.S. Meat Animal Research Center, Clay Center, Nebraska. Further description of the lamb mortality records used in the present analysis can be found in Southey et al. (2001), and the population and management were described by Leymaster (1991) and Mousa et al. (1999).

Lamb records were available from 1985 through 1997 with the date and cause of mortality determined by necropsy for lambs that died. Records from lambs that lost their identification were removed from the data prior to any analysis since the status of these lambs was unknown for any of the ages considered. After approximately 20 wk of age, the culling of surplus lambs from the main flock started on a regular basis and culled lambs were treated as censored on the day of culling. The pedigree consisted of 8,642 lambs from 299 sires and 2,475 dams. Analyses were conducted on three periods: birth to weaning, weaning to 365 d of age, and birth to 365 d of age with mortality rates of 15.2, 7.6, and 21.6%, respectively.

Animal–time data sets were created for each period using different durations of time intervals and actual survival age as described by Allison (1997). The resulting data sets consisted of a binary response variable that indicated either occurrence or nonoccurrence of mortality for each discrete time interval observed for each animal in every period. Two cases illustrate the data structure: In the first case, an animal that is alive for four time intervals would have four nonoccurrence mortality observations, one for each of the four time intervals. In the second case, an animal that was only alive for two periods would have only two records, where the first time interval is recorded as a nonoccurrence of mortality and the second time interval is recorded as an occurrence of mortality. Within all periods, time interval durations of weeks and fortnights were analyzed. In addition, a daily duration time interval was studied for birth to weaning and a monthly duration time interval was studied for weaning to 365 d of age and birth to 365 d of age.

Statistical Methods

The animal–time data sets were analyzed by modeling the discrete hazard function, $\lambda(t_i)$, with k explanatory variables for each animal:

$$\lambda(t_i) = g\left(\sum_{j=1}^{k} x_{ij}\beta_j\right) \quad [1]$$

where t_i is the observed time of mortality of the ith animal, $g(\cdot)$ is a link function, x_{ij} is the jth explanatory variable for the ith animal, and β_j is the regression coefficient associated with the jth explanatory variable. This model results from the equivalence between the discrete time survival likelihood and the likelihood from a binary response model (Fahrmeir and Tutz, 1994). An alternative perspective follows from the definition of the conditional probabilities (Allison, 1997). The discrete hazard function or conditional probability for the risk of mortality given that the time interval is reached is given by:

$$\lambda(t_i) = \Pr(T_i = t_i | T_i > t_i)$$

where $T_i = t_i$ denotes mortality within the time interval (Fahrmeir and Tutz, 1994; Allison, 1997). The conditional probability of mortality given that the time interval is reached can be factored into the product of conditional probabilities:

$$\Pr(T_i = t_i | T_i > t_i) = P_{t_i} \sum_{u=1}^{t_i-1} (1 - P_u) \quad [2]$$

where P_{t_i} and P_u are conditional probabilities of mortality given that no mortality has occurred at time t_i and u, respectively. Consequently, each right hand side term in Eq. [2] is treated as resulting from independent observations from each animal (Allison, 1997), thus permitting the use of Eq. [1].

Two link functions, the logistic and complementary log–log functions, were evaluated. These functions specify models with different metrics, and hence interpretations, since the logistic function provides a proportional odds model and the complementary log–log function provides a proportional hazards model (Allison, 1997). Duration of time interval was included as a discrete classification in all analyses due to model differences associated with using these link functions. The complementary log–log model is invariant to the duration of the time interval, whereas the logistic model is variant to the duration of the time interval; hence, the logistic model coefficients are not directly comparable across time intervals of different durations (Allison, 1997). In addition, the Weibull model is represented in the complementary log–log model when the natural log of the duration of the time interval is fitted as a covariate (Allison, 1997). In this study, preliminary analysis combined with the results of Southey et al. (2001) indicated that the Weibull model would provide an adequate fit to the data in this study (Figures 1, 2, and 3), but was not considered in order to compare results from both link functions.

Other explanatory variables considered in all models were sex (two levels: male and female), type of birth

Table 1. Hazard ratios and approximate standard errors of the explanatory variables from birth to weaning using a complementary log-log sire model and different durations of time interval

Effect[a]	Duration of time interval		
	Daily	Weekly	Fortnightly
Lamb sex			
M-F	1.23 ± 0.07	1.23 ± 0.07	1.23 ± 0.07
Type of birth			
S-M	0.30 ± 0.03	0.30 ± 0.03	0.30 ± 0.03
T-M	0.47 ± 0.04	0.47 ± 0.04	0.48 ± 0.04
Age of dam			
1-4	2.97 ± 0.38	2.94 ± 0.37	2.94 ± 0.37
2-4	1.42 ± 0.16	1.41 ± 0.16	1.41 ± 0.16
3-4	0.85 ± 0.10	0.85 ± 0.10	0.85 ± 0.10
Nursery			
N-Y	0.70 ± 0.08	0.70 ± 0.08	0.70 ± 0.08

[a]M-F = effect of male lambs as deviation from female lambs; S-M = effect of single-born lambs as a deviation from multiple-born lambs; T-M = effect of twin-born lambs as a deviation from multiple-born lambs; 1-4 = effect of 1-yr-old ewes as a deviation of 4-yr or older ewes; 2-4 = effect of 2-yr-old ewes as a deviation of 4-yr or older ewes; 3-4 = effect of 3-yr-old ewes as a deviation of 4-yr or older ewes; N-Y = effect of lambs not raised in nursery as a deviation of lambs raised in nursery.

Table 2. Hazard ratios and approximate standard errors of the explanatory variables from weaning to 365 d of age using a complementary log–log sire model and different durations of time interval

Effect[a]	Duration of time interval		
	Weekly	Fortnightly	Monthly
Lamb sex			
M-F	1.40 ± 0.19	1.37 ± 0.19	1.26 ± 0.17
Type of birth			
S-M	0.91 ± 0.23	0.89 ± 0.23	0.88 ± 0.22
T-M	0.72 ± 0.16	0.71 ± 0.16	0.70 ± 0.15
Age of dam			
1-4	0.87 ± 0.26	0.88 ± 0.26	0.88 ± 0.26
2-4	0.95 ± 0.23	0.95 ± 0.23	0.96 ± 0.24
3-4	1.12 ± 0.26	1.12 ± 0.26	1.13 ± 0.27
Nursery			
N-Y	0.63 ± 0.20	0.59 ± 0.19	0.59 ± 0.18

[a]M-F = effect of male lambs as deviation from female lambs; S-M = effect of single-born lambs as a deviation from multiple-born lambs; T-M = effect of twin-born lambs as a deviation from multiple-born lambs; 1-4 = effect of 1-yr-old ewes as a deviation of 4-yr or older ewes; 2-4 = effect of 2-yr-old ewes as a deviation of 4-yr or older ewes; 3-4 = effect of 3-yr-old ewes as a deviation of 4-yr or older ewes; N-Y = effect of lambs not raised in nursery as a deviation of lambs raised in nursery.

(three levels: single, twin, and multiple), contemporary group (18 levels), age of dam (four levels: 1, 2, 3, and 4+ yr old), and nursery code (two levels: Y if a lamb was raised in the nursery and N otherwise). Contemporary group was defined as the year of lambing and one of two 35-d breeding periods within year when relevant. Sire, animal, and maternal effects models were fitted using ASREML (Gilmour et al., 1999). Heritabilities were calculated using the variances of the link functions: $\pi^2/3$ and $\pi^2/6$ for the logistic and complementary log–log link functions, respectively (Fahrmeir and Tutz, 1994).

Results

Estimates of explanatory variables were very similar between sire, animal, and maternal effects models fitted for each period using different link functions. Consequently, only hazard ratios from explanatory variables using sire models are presented in Tables 1, 2, and 3 for the periods from birth to weaning, birth to 365 d of age, and weaning to 365 d of age, respectively. Adjusted probabilities of mortality for each period (Figures 1, 2, and 3) illustrate the similarity of the link functions.

Within each period, the duration of the time interval generally showed similar estimates regardless of the actual unit of time used. Figures 1, 2, and 3 also illustrate the lack of influence of the duration of time interval when the adjusted probabilities of mortality were compared to a cumulative probability from time interval with shorter durations. Mortality probability peaked at the end of the periods in each Figure and is due to accumulation of time intervals with few mortality records. The estimates from the period of weaning

to 365 d of age (Figure 2) showed a smaller trend across time interval of different durations and large standard errors compared to the other periods. This trend can be attributed to the few mortality records and high degree of censoring since this trend was not observed in the other periods.

In the period from birth to weaning (Table 1), male lambs had 23% greater hazard of mortality than female.

Table 3. Hazard ratios and approximate standard errors of the explanatory variables from birth to 365 d of age using a complementary log–log sire model and different durations of time interval

Effect[a]	Duration of time interval		
	Weekly	Fortnightly	Monthly
Lamb sex			
M-F	1.23 ± 0.06	1.24 ± 0.06	1.23 ± 0.06
Type of birth			
S-M	0.42 ± 0.04	0.42 ± 0.04	0.43 ± 0.04
T-M	0.55 ± 0.04	0.55 ± 0.04	0.55 ± 0.04
Age of dam			
1-4	2.43 ± 0.26	2.44 ± 0.26	2.45 ± 0.26
2-4	1.34 ± 0.13	1.34 ± 0.13	1.35 ± 0.13
3-4	0.95 ± 0.09	0.95 ± 0.09	0.95 ± 0.09
Nursery			
N-Y	0.49 ± 0.04	0.47 ± 0.04	0.47 ± 0.04

[a]M-F = effect of male lambs as deviation from female lambs; S-M = effect of single-born lambs as a deviation from multiple-born lambs; T-M = effect of twin-born lambs as a deviation from multiple-born lambs; 1-4 = effect of 1-yr-old ewes as a deviation of 4-yr or older ewes; 2-4 = effect of 2-yr-old ewes as a deviation of 4-yr or older ewes; 3-4 = effect of 3-yr-old ewes as a deviation of 4-yr or older ewes; N-Y = effect of lambs not raised in nursery as a deviation of lambs raised in nursery.
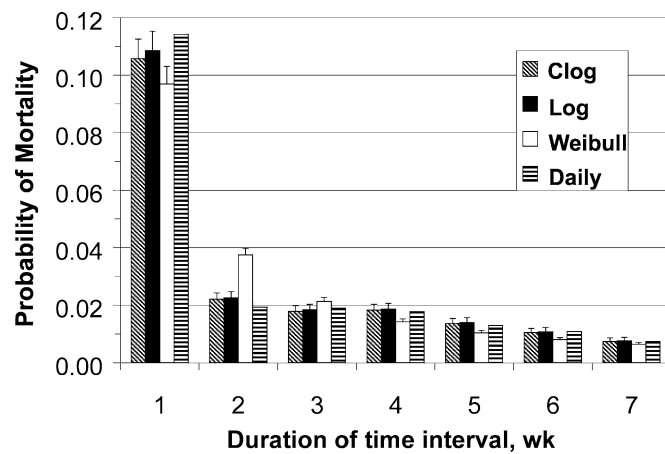
Figure 1. Adjusted probabilities (and SE) of lamb mortality over weekly time intervals from birth to weaning using complementary log–log (Clog), logistic (Log), and Weibull sire models compared to cumulative daily time intervals (Daily) from birth to weaning using a Clog sire model.

Single and twin lambs had 70 and 53% lower hazard of mortality than multiple-born lambs, respectively. Lambs from 1- and 2-yr-old dams had significantly ($P < 0.01$) greater hazard of mortality (194 and 41%, respectively using a weekly duration) than lambs from 4-yr-old and older dams. Lambs from 3-yr-old dams had a 15% lower hazard of mortality than lambs from 4-yr-old and older dams, although this was nonsignificant. Lambs raised with their dams had an approximately 30% lower hazard of mortality than lambs raised in the nursery.

Similar interpretations of the birth to weaning period are applicable to the weaning to 365 d of age period
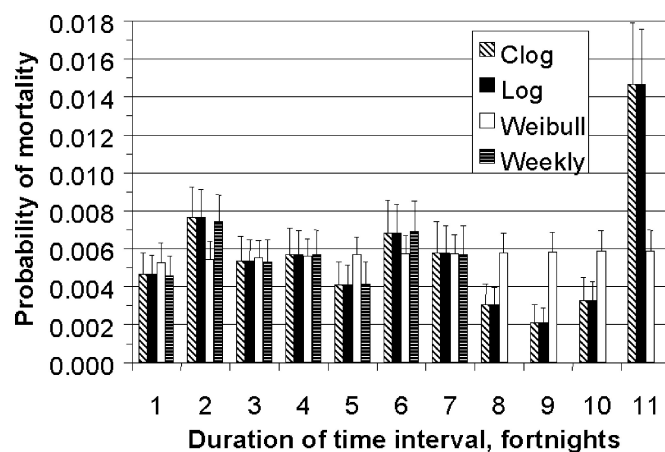

Figure 2. Adjusted probabilities (and SE) of lamb mortality over fortnightly time intervals from weaning to 365 d of age using complementary log–log (Clog), logistic (Log), and Weibull sire models compared to cumulative weekly time intervals (Weekly) from weaning to 365 d of age using a Clog sire model.
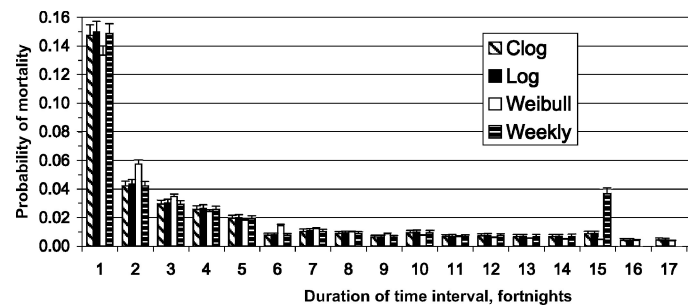

Figure 3. Adjusted probabilities (and SE) of lamb mortality over fortnightly time intervals from birth to 365 d of age using complementary log–log (Clog), logistic (Log), and Weibull sire models compared to cumulative weekly time intervals (Weekly) from birth to 365 d of age using a Clog sire model.

(Table 2) and birth to 365 d of age period (Table 3). The estimates from the birth to 365 d of age period were, in general, more similar to the birth to weaning period than to the weaning to 365 d of age period. For the period from weaning to 365 d of age, reduced and nonsignificant differences due to type of birth and age of dam were observed compared with the other periods. The influence of lamb sex in the weaning to 365 d of age period was greater than the other periods, although this decreased with greater durations. This result is likely due to few mortality records in this period since the monthly time interval values were closer to the other periods. The hazard of mortality due to nursery raising was increased slightly in the weaning to 365 d of age period, and this resulted in lambs raised by their dams having a 41% hazard of mortality for lambs raised in the nursery in the period using either fortnightly or monthly durations from the birth to weaning period.

Estimates of sire, additive genetic and maternal variances, and the covariance between additive genetic and maternal effects were very similar between link functions and different durations of time interval in the birth to weaning (Table 4) and birth to 365 d of age (Table 5) periods. In the weaning to 365 d of age period, no maternal effects were detected and sire and additive genetic effects were similar across link functions and durations of time intervals (Table 6). Correlations between breeding values were typically greater than 99% across link functions and different durations of time intervals, indicating that the same group of individuals would be selected to improve lamb mortality. For example, from birth to weaning, the same top 10 sires were identified across the different link functions and time interval durations.

Heritability estimates in the complementary log–log analysis were approximately double the estimates in the logistic analysis for all periods and time interval durations. This result is expected since the variance of the complementary log–log function is half the variance of the logistic function. Sire-model heritability esti-

Table 4. Variance components and heritability estimates from birth to weaning with different durations of time interval using a discrete survival model with logistic or complementary log–log (Clog) link function

	Duration of time interval					
	Daily		Weekly		Fortnightly	
	Logistic	Clog	Logistic	Clog	Logistic	Clog
Sire effects model						
Sire variance	0.080 ± 0.027	0.080 ± 0.026	0.081 ± 0.028	0.079 ± 0.026	0.082 ± 0.029	0.077 ± 0.026
Heritability	0.096 ± 0.031	0.185 ± 0.058	0.096 ± 0.032	0.184 ± 0.057	0.097 ± 0.033	0.179 ± 0.057
Animal effects model						
Additive genetic variance	0.219 ± 0.073	0.224 ± 0.071	0.193 ± 0.071	0.195 ± 0.066	0.183 ± 0.070	0.183 ± 0.064
Heritability	0.062 ± 0.020	0.120 ± 0.034	0.055 ± 0.019	0.106 ± 0.032	0.053 ± 0.019	0.100 ± 0.031
Maternal effects model						
Additive genetic variance (A)	0.186 ± 0.085	0.187 ± 0.082	0.161 ± 0.082	0.165 ± 0.077	0.149 ± 0.082	0.152 ± 0.074
Maternal variance (M)	0.306 ± 0.094	0.309 ± 0.092	0.286 ± 0.093	0.291 ± 0.088	0.274 ± 0.093	0.277 ± 0.085
Covariance (A, M)	−0.167 ± 0.085	−0.166 ± 0.083	−0.151 ± 0.083	−0.157 ± 0.079	−0.141 ± 0.083	−0.147 ± 0.076
Additive genetic heritability	0.054 ± 0.025	0.103 ± 0.046	0.047 ± 0.024	0.092 ± 0.043	0.044 ± 0.024	0.085 ± 0.042
Maternal heritability	0.089 ± 0.028	0.171 ± 0.053	0.083 ± 0.028	0.163 ± 0.051	0.080 ± 0.027	0.156 ± 0.050
Correlation (A, M)	−0.699 ± 0.205	−0.694 ± 0.202	−0.702 ± 0.226	−0.718 ± 0.208	−0.696 ± 0.242	−0.716 ± 0.217

mates were greater than those from animal and maternal effects models, although these models are not linearly equivalent. This difference could be attributed to overdispersion since three quarters of the additive genetic variance is unaccounted for in the sire model compared to the animal and maternal models. Heritability estimates were slightly higher in the animal model than in the maternal effects model. This result could be associated with some of the variability between animals being due to maternal effects. Estimates of the correlation between direct additive and maternal effects were similar across periods and time-interval durations since the correlation does not depend on the variance of the link function.

Discussion

The implemented discrete time survival analysis provided an alternative approach to the mortality study than that undertaken by Southey et al. (2001). Estimates of the explanatory variables reported by Southey et al. (2001) using continuous time survival models were very similar to those obtained in this study. This result was expected since Ingram and Kleinman (1989) also empirically showed that the similarity between proportion hazards and logistic models assuming that there were no differential censoring rates within explanatory variables. More formally, Doskum and Gasko (1990) proved the direct correspondence between binary data analysis and continuous time survival analysis.

The estimates of the sire variance in this study were very similar to corresponding estimates reported by Southey et al. (2001). Estimates of the sire variance in the birth to weaning and birth to 365 d of age periods using a discrete time approach were lower than the estimates for the same periods using Weibull and Logistic sire models reported by Southey et al. (2001). In the weaning to 365 d of age period, the estimates from the

Table 5. Variance components and heritability estimates from birth to 365 d of age with different durations of time interval using a discrete survival model with logistic or complementary log–log (Clog) link function

	Duration of time interval					
	Weekly		Fortnightly		Monthly	
	Logistic	Clog	Logistic	Clog	Logistic	Clog
Sire effects model						
Sire variance	0.058 ± 0.019	0.057 ± 0.019	0.058 ± 0.020	0.055 ± 0.018	0.060 ± 0.021	0.055 ± 0.018
Heritability	0.069 ± 0.023	0.133 ± 0.042	0.069 ± 0.023	0.130 ± 0.042	0.072 ± 0.024	0.130 ± 0.042
Animal effects model						
Additive genetic variance	0.168 ± 0.054	0.164 ± 0.051	0.162 ± 0.053	0.157 ± 0.050	0.153 ± 0.053	0.142 ± 0.047
Heritability	0.049 ± 0.015	0.091 ± 0.026	0.047 ± 0.015	0.087 ± 0.025	0.044 ± 0.015	0.079 ± 0.024
Maternal effects model						
Additive genetic variance (A)	0.144 ± 0.064	0.141 ± 0.061	0.137 ± 0.064	0.132 ± 0.059	0.128 ± 0.064	0.119 ± 0.057
Maternal variance (M)	0.191 ± 0.065	0.194 ± 0.062	0.181 ± 0.064	0.184 ± 0.061	0.172 ± 0.064	0.169 ± 0.058
Covariance (A, M)	−0.111 ± 0.059	−0.113 ± 0.057	−0.103 ± 0.059	−0.104 ± 0.055	−0.096 ± 0.059	−0.095 ± 0.053
Direct heritability	0.042 ± 0.019	0.080 ± 0.035	0.040 ± 0.019	0.075 ± 0.034	0.038 ± 0.019	0.068 ± 0.032
Maternal heritability	0.056 ± 0.019	0.110 ± 0.036	0.053 ± 0.019	0.105 ± 0.035	0.051 ± 0.019	0.097 ± 0.034
Correlation (A, M)	−0.669 ± 0.208	−0.682 ± 0.199	−0.654 ± 0.220	−0.665 ± 0.210	−0.648 ± 0.236	−0.669 ± 0.221

Table 6. Variance components and heritability estimates from weaning to 365 d of age with different durations of time interval using a discrete survival model with logistic or complementary log-log (Clog) link function

| | Duration of time interval | | | | | |
| | Weekly | | Fortnightly | | Monthly | |
Link	Logistic	Clog	Logistic	Clog	Logistic	Clog
Sire effects model						
Sire variance	0.090 ± 0.088	0.090 ± 0.087	0.088 ± 0.087	0.088 ± 0.087	0.087 ± 0.088	0.087 ± 0.086
Heritability	0.107 ± 0.101	0.207 ± 0.190	0.104 ± 0.101	0.203 ± 0.190	0.104 ± 0.101	0.201 ± 0.190
Animal effects model						
Additive genetic variance	0.191 ± 0.203	0.192 ± 0.201	0.188 ± 0.202	0.190 ± 0.201	0.185 ± 0.202	0.189 ± 0.200
Heritability	0.055 ± 0.055	0.105 ± 0.098	0.054 ± 0.055	0.103 ± 0.098	0.053 ± 0.055	0.103 ± 0.098

discrete time approach were higher than the estimates from Weibull and Logistic sire models reported by Southey et al. (2001). The difference in heritability estimates between the logistic sire models and the Weibull and complementary log–log sire models corresponds to the difference in the link function variance. Greater estimates of the additive genetic and maternal variances, and consequently, greater heritability estimates, were observed in the discrete time logistic models than the cumulative logistic animal model of Southey et al. (2001).

The similarity of estimates between logistic and complementary log–log models is expected since these functions have very similar properties at the range of mortalities observed in the data set (Fahrmeir and Tutz, 1994). In addition, both the logistic and complementary log–log models can be derived from the Cox proportional hazards model as a first-order approximation (Cox, 1972; Kalbfleisch and Prentice, 1973). Although Cox (1972) proposed the logistic model as an approximation, coefficients from a complementary log–log model have the same relative risk interpretation as the Cox proportional hazards model (Kalbfleisch and Prentice, 1973; Allison, 1997). However, the logistic and complementary log–log models differed from the Cox proportional hazards model estimates reported by Southey et al. (2001).

Lower estimates from the Cox proportional hazards model compared to Weibull or discrete–time sire models are probably associated with the different modeling of the information contained by the data since the Cox proportional hazards model uses the marginal distribution of ranks (Kalbfleisch and Prentice, 1973). Assuming a log-linear hazard rate, the appropriate distribution for the Cox proportional hazards model is the extreme-value distribution (Kalbfleisch and Prentice, 1973; Doksum and Gasko, 1990). Consequently, using the extreme-value distribution function, heritability estimates from the Cox proportional hazards sire model are lower than estimates from the Weibull and complementary log–log sire models, but greater than estimates from the logistic sire models. More generally, given an unspecified baseline hazard function, the Cox proportional hazards model is a linear transformation model

with an unknown transformation (Doksum and Gasko, 1990; Fahrmeir and Tutz, 1994). Since the Cox proportional hazards model is distribution free, Kent and O'Quigley (1988) proposed using a value of one when computing the proportion of variance explained by the Cox proportional hazards model. Yadzi et al. (2002) also suggested a value of one based on the definition of reliability under selection index and mixed-model theory. Using this value to compute heritability instead of 1.64 ($\pi^2/6$) would result in greater heritability estimates, although all models would still have similar variance component estimates.

The approach used in this study involved the grouping of a continuous variable into discrete time intervals. This is expected to result in a loss of information since the likelihood factors into the product of the conditional independent periods (Fahrmeir and Tutz, 1994). Gould and Lawless (1988) showed that the loss of information has a minimal effect on efficiency of estimation that is similar with results reported in this study. When comparing time intervals with different durations, the additional information added does not change the standard errors of estimates (Allison, 1997). Therefore, the similarity of results from the discrete time models to the continuous time models was expected and illustrates that the discrete time analysis is a valid alternative approach in this data set.

In the present analysis, the time intervals were assumed and treated as independent. Xu and Brookmeyer (1997) proved that this approach could be applied to each time point provided that for each point, the expected value of the product of contributions for each time interval is the same as the product of expected values of each time interval. The consistencies of the explanatory effects and sire variance estimates between the continuous- and discrete-time sire models appear to validate this result. Estimates of variance components that generally decreased when duration was increased, particularly for the animal and maternal effects models. However, standard errors also decreased, indicating this was directly associated with information content since the greater durations incorporated more mortality records than the lesser durations.

Experimental results presented in this study and by Southey et al. (2001) provide examples of the theoretical relationships between different approaches to model survival data, such as mortality and longevity. Discrete and continuous time approaches are generally expected to provide similar results if exact time of mortality is known. When the exact time of mortality is unknown, the results from Ingram and Kleinman (1989) and this study indicate that the discrete approach will provide results similar to those when the exact time of mortality is known. The cumulative binary approach also provided similar estimates in this data set, but required additional assumptions to address censoring (Southey et al., 2001). Larger differences between the approaches than the ones seen in this study are expected with greater mortality rates and differential censoring, although Ingram and Kleinman (1989) showed that the discrete- and continuous-time approaches provided similar results in these situations.

Implications

Results of this study indicate that discrete-time survival methods are a viable alternative to continuous-time survival methods to estimate fixed effects and variance components. The suitability of cumulative-binary, continuous-time, and discrete-time approaches depends on the data structure analyzed and the model assumptions. The similarity of the results suggests that cumulative-binary, continuous-time, and discrete-time approaches can be used to analyze lamb mortality and other survival data.

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